



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/963,668

Source:

OIPE

Date Processed by STIC:

10/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIKE

RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/963,668

TIME: 10:56:12

Input Set : A:\000425 BTe AL1_Dpckaec.app

Output Set: N:\CRF3\10102001\I963668.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Degussa AG
 5 <120> TITLE OF INVENTION: Process for the fermentative preparation of
 6 L-amino acids using strains of the
 7 Enterobacteriaceae family.
 9 <130> FILE REFERENCE: 000425 BT
 11 <140> CURRENT APPLICATION NUMBER: US/09/963,668
 12 <141> CURRENT FILING DATE: 2001-09-27
 14 <160> NUMBER OF SEQ ID NOS: 19
 16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1622 1623 (p.3)
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Escherichia coli
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(1620)
 26 <223> OTHER INFORMATION: pckA
 28 <400> SEQUENCE: 1
 29 atg cgc gtt aac aat ggt ttg acc ccg caa gaa ctc gag gct tat ggt 48
 30 Met Arg Val Asn Asn Gly Leu Thr Pro Gln Glu Leu Glu Ala Tyr Gly
 31 1 5 10 15
 33 atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg 96
 34 Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
 35 20 25 30
 37 tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg 144
 38 Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
 39 35 40 45
 41 tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt 192
 42 Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
 43 50 55 60
 45 cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat 240
 46 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
 47 65 70 75 80
 49 act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct 288
 50 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
 51 85 90 95
 53 ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag 336
 54 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
 55 100 105 110
 57 ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac 384
 58 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
 59 115 120 125
 62 ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag 432

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63 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
64      130                      135                      140
66 gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg      480
67 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
68 145.                      150                      155                      160
70 gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act      528
71 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
72                      165                      170                      175
74 aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg      576
75 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
76                      180                      185                      190
78 ttt aac ctg acc gag cgc atg cag ctg att ggc ggc acc tgg tac ggc      624
79 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
80                      195                      200                      205
82 ggc gaa atg aag aaa ggg atg ttc tcg atg atg aac tac ctg ctg ccg      672
83 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
84      210                      215                      220
86 ctg aaa ggt atc gct tct atg cac tgc tcc gcc aac gtt ggt gag aaa      720
87 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
88 225                      230                      235                      240
90 ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc      768
91 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
92                      245                      250                      255
94 ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc      816
95 Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
96                      260                      265                      270
98 tgg gac gat gac ggc gtg ttt aac ttc gaa ggc ggc tgc tac gca aaa      864
99 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
100                      275                      280                      285
102 act atc aag ctg tcg aaa gaa gcg gaa cct gaa atc tac aac gct atc      912
103 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
104      290                      295                      300
106 cgt cgt gat gcg ttg ctg gaa aac gtc acc gtg cgt gaa gat ggc act      960
107 Arg Arg Asp Ala Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
108 305                      310                      315                      320
110 atc gac ttt gat gat ggt tca aaa acc gag aac acc cgc gtt tct tat      1008
111 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
112                      325                      330                      335
114 ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc      1056
115 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
116                      340                      345                      350
118 cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg      1104
119 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
120                      355                      360                      365
123 ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc      1152
124 Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
125      370                      375                      380
127 tct ggc ttc acc gcc aaa ctg gcc ggt act gag cgt ggc atc acc gaa      1200
128 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu

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129 385          390          395          400
131 ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg 1248
132 Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
133          405          410          415
135 cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg 1296
136 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
137          420          425          430
139 ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa 1344
140 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
141          435          440          445
143 cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac 1392
144 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
145          450          455          460
147 ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg 1440
148 Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
149 465          470          475          480
151 gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg 1488
152 Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
153          485          490          495
155 cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc 1536
156 Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
157          500          505          510
159 ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct 1584
160 Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
161          515          520          525
163 gcg ggt gcc gcg ctg gta gcg gct ggt ccg aaa ctg taa
164 Ala Gly Ala Ala Leu Val Ala Ala Gly Pro Lys Leu
E--> 165          530          535          540

```

1623

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,668

DATE: 10/10/2001

TIME: 10:56:13

Input Set : A:\000425 BTe AL1_Dpckaec.app

Output Set: N:\CRF3\10102001\I963668.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:165 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1622 Found:1623 SEQ:1